

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 16, 2003 16:40:32 - Search time 43 7143 seconds
(without alignments)
56.562 Million cell updates/sec

Title: US-09-856-070-21

Perfect score: 60

Sequence: 1 FELMLRLQDYEE 12

Scoring table: RLSUM62

Gapop 10 0, Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_viruses:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	60	100.0	586	4	Q96C08	Q96C08 homo sapien
2	57	95.0	159	4	Q9UJ26	Q9UJ26 homo sapien
3	57	95.0	586	11	Q9UC11	Q9UC11 mys musculu
4	55	91.7	158	4	Q9UJ27	Q9UJ27 homo sapien
5	53	88.3	455	11	Q9V4K3	Q9V4K3 rattus norv
6	45	75.0	585	14	Q9V3W6	Q9V3W6 gallus gall
7	40	66.7	534	14	Q9QXY5	Q9QXY5 tigr rubrif
8	39	65.0	250	17	Q9HR00	Q9HR00 halobacteri
9	39	65.0	376	5	Q95QW7	Q95QW7 caenorhabd
10	39	65.0	429	4	P78514	P78514 homo sapien
11	39	65.0	453	4	Q99854	Q99854 homo sapien
12	39	65.0	584	15	Q55449	Q55449 synetocyst
13	39	65.0	634	9	Q9XJ53	Q9XJ53 bacterioph
14	34	66.0	402	16	Q9V4K2	Q9V4K2 homo sapien
15	38	63.3	47	16	Q9V4K2	Q9V4K2 arabidopsi
16	38	63.3	130	16	Q9K660	Q9K660 bacillus ha

Q8UHE2 agrobacteri
Q95W18 macaca fasc
Q8W20 macaca fasc
Q9M50 homo sapien
Q91480 salmo salar
Q81517 anopheles q
Q20766 caenorhabd
Q64706 bacterioph
Q34838 bacillus su
Q45212 bromia faja
Q9UJ28 homo sapien
Q9V29 homo sapien
Q8152 pyrococcus
Q840V8 pyrococcus
Q9217 pyrococcus
Q81900 aedes aegypt
Q52534 pseudomonas
Q9P9S2 xylicella fas
Q65941 aquifex aco
Q81366 drosophila
Q9V4P8 drosophila
Q91748 xenopus lae
Q8W45 ectocarpus
Q9X28 streptomyce
Q974U8 sulfolobus
Q85V28 encephalito
Q9H242 pseudomonas
Q9ZU1 arabidopsis
P78849 schizosacch

ALIGNMENTS

RESULT 1

Q96C08
ID Q96C08 PRELIMINARY; PRT: 586 AA.
AC Q96C08
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
OS Similar to villin 2 (ezrin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
FI Submitted (SEP 2001) to the EMBL/GenBank/DBJ databases
DR EMBL: BC013903; AAI13903.1; -;
DR InterPro: IPR000299; Band_4.1;
DR InterPro: IPR000798; Pz/rad/moesin.
DR Pfam: PF00373; Band_4.1; 1;
DR Pfam: PF00769; ERM; 1;
DR PROSITE: PS00660; BAND_4.1; UNKNOWN_1;
DR PROSITE: PS00661; BAND_4.1; UNKNOWN_1;
DR PROSITE: PS00057; BAND_4.1; 1;
SQ SEQUENCE 586 AA; 59412 MW; F1B592CF49A7CC46 CRC64;

Query Match 100.0%; Score 60; DB 4; Length 586;

Best Local Similarity 100.0%; Pred NC: 0.012; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0;

QY 1 FELMLRLQDYEE 12

DB 345 FELMLRLQDYEE 356

RESULT 2

Q9UJ26

ID Q9UJ26 PRELIMINARY; PRT: 159 AA.

Q9DJZ6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fadiel A., Chen Z.C., Nattoli F.;
 RT "Mutation of ezrin gene in cancer.";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF189213; AAF03156.1; -;
 DR InterPro: IPK000299; Hand.4.1.
 DR InterPro: IPK000798; Ez/rad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 19234 MW; 7C398388B7HA70FA CRC64;
 Query Match 95.0%; Score 57; DB 4; Length 159;
 Best Local Similarity 91.7%; Pred. No. 0.011;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FELMLRLQDYEE 12
 DB 148 FELMLRLQDYED 159
 RESULT 3
 Q9DC11
 DI Q9DC11 PRELIMINARY; PRI: 586 AA.
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Adult male kidney cDNA, RIKEN full-length enriched library,
 DE clone:0610037H22, full insert sequence.
 GN VIL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN:57RL/6J; TISSUE-KIDNEY;
 FX MEDLINE-2105660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Niyasawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., Kiss B., Kochiwa H.,
 RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi P., Stambli P., Suzuki K., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Bellelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Rind B., Ringwald M., Rodriguez J., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Bayazitkazi Y.;
 RI "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK02265; BAB22341.1; -;
 DR MGD: MGI:98931; VIL2.
 DI InterPro: IPR000249; Band_41.1.

DR InterPro: IPK000798; Ez/rad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PR00935; HAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 SQ SEQUENCE 586 AA; 69434 MW; 591AH8F575F6DE3E CRC64;
 Query Match 95.0%; Score 57; DB 11; Length 586;
 Best Local Similarity 91.7%; Pred. No. 0.041;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FELMLRLQDYEE 12
 DB 345 FELMLRLQDYEQ 356
 RESULT 4
 Q9UJZ7
 DI Q9UJZ7 PRELIMINARY; PRI: 158 AA.
 AC Q9UJZ7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAP-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen Z.C., Fadiel A., Nattoli F.;
 RT "Ezrin gene mutation in ovarian cancer.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF188897; AAF03155.1; -;
 DR InterPro: IPK030299; Hand.4.1.
 DR InterPro: IPK000798; Ez/rad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 FT NON_TER 1
 FT NON_TER 158
 SQ SEQUENCE 158 AA; 19086 MW; 86F92E1HC6F2957E CRC64;
 Query Match 91.7%; Score 55; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FELMLRLQDYEE 11
 DB 148 FELMLRLQDYEE 158
 RESULT 5
 Q8VHK3
 DI Q8VHK3 PRELIMINARY; PRI: 455 AA.
 AC Q8VHK3;
 DT 01-MAP-2002 (TrEMBLrel. 20, Created)
 DI 01-MAP-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ezrin (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN:SPRAGUE-DAWLEY;
 RA Gunn Moore P.J., Tait S., Prophy P.J.;
 PL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF450298; AAL47844.1; -;


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ID Q99QW7 PRELIMINARY: PRT: 476 AA.
AC Q99QW7;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DI 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 44.4 kDa protein.
GN C14F5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Polodermidae; Caenorhabditis.
OX NCBI_TaxID=6239.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
FX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Mix P.;
RT "The sequence of C. elegans cosmid C14F5.3";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: 024082; AAC02434.1; -.
KW Hypothetical protein.
SQ SEQUENCE 376 AA; 44436 MW; 93832C5H13C4A6CE CRC64;

Query Match 65.0%; Score 39; DB 5; Length 376;
Best Local Similarity 72.7%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 12
II :|||||
Ib 92 EEQAKLQVEE 103

RESULT 10
P78514
ID P78514 PRELIMINARY: PRT: 429 AA.
AC P78514; Q99B44;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DI 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DE 01-MAY-1997 (TEMBLrel. 03, Last annotation update)
DE Hypothetical 48.1 kDa protein (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Keen T.J.;
RT "Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL: 085995; AAB61919.1; -.
DR EMBL: 085994; AAB61918.1; -.
DR EMBL: 085997; AAB6606.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 429 AA; 48092 MW; D8E2471A5971E9A CRC64.

Query Match 65.0%; Score 39; DB 4; Length 429;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ELMRLQDYEE 12

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II :|||||
Ib 157 ELILRLQVEE 167

RESULT 11
Q99B54
ID Q99B54 PRELIMINARY: PRT: 453 AA.
AC Q99B54;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DI 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Hypothetical 51.1 kDa protein (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA Keen T.J.;
RT "Positional candidates for the RP9 retinitis pigmentosa gene.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 087408; AAB47568.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 453 AA; 51050 MW; C5F53EE64A841418 CRC64.

Query Match 65.0%; Score 39; DB 4; Length 453;
Best Local Similarity 72.7%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ELMRLQDYEE 12
II :|||||
Ib 181 ELILRLQVEE 191

RESULT 12
Q55449
ID Q55449 PRELIMINARY: PRT: 584 AA.
AC Q55449;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DI 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Hypothetical protein sir0031.
GN SIR0031.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC 6803;
RA Tabata S.;
RT Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=97061201; PubMed=8905211;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasaki S., Kimura T.,
RA Hosouchi T., Matsuoka A., Muraki A., Nakazaki N., Narino K., Okumura S.,
RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein coding regions.";

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RL DNA Res. 3:109-136(1996).
 DR EMBL: D64006; BAAL0791.1; -
 DR MROPS; M61.001; -
 DR InterPro: IPR001478; P0V.
 DR InterPro: IPR00130; Zn_MiPeptdse.
 DR Pfam: PF00595; PDZ_1.
 DR SMART: SM00228; PDZ_1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 584 AA; 65.0% MW: 64810096.44284847 GC241

Query Match 65.0% Score 39; DB 16; Length 584;
 Best Local Similarity 63.6% Pred. No. 78;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 1 EELMLRLQDYE 11
 I:|||||
 Db 521 EQLSLRLKDYQ 531

RESULT 13

Q9XJS3 PRELIMINARY; PROT; 634 AA.

AC Q9XJS3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Putative replication initiation protein p12.
 OS Bacteriophage PM2.
 OS Bacteriophage PM2.
 OS Viruses; dsDNA viruses, no RNA stage; Corticoviridae; Corticovirus.
 OC NCBI_TaxID=10661;
 RL [1]
 RP SEQUENCE FROM N.A.
 RA Kivela H.M., Mannisto R.H., Kalkbrenner N., Hamford J.K.H.;
 RT "Purification and protein composition of PM2, the first lipid-
 containing bacterial virus to be isolated.";
 RL Virology 0-0-0(1999)
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99434236; PubMed=10502514;
 RA Mannisto R.H., Kivela H.M., Paulin L., Hamford J.K.H.;
 RT "The complete genome sequence of PM2, the first lipid containing
 bacterial virus to be isolated.";
 RL Virology 262:355-363(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Mannisto R.H., Kivela H.M., Paulin L., Hamford J.K.H.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases
 DR EMBL: AF155037; AAD43543.1; -
 SQ SEQUENCE 634 AA; 72.094 MW: 65610000.4FEB2506 GP054

Query Match 65.0% Score 39; DB 9; Length 634;
 Best Local Similarity 63.6% Pred. No. 85;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 2 EELMLRLQDYE 12
 I:|||||
 Db 275 FIMWPIPGYEF 285

RESULT 14

Q9Y699 PRELIMINARY; PROT; 802 AA.

AC Q9Y699;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PRH-responsive osteosarcoma B1 protein.
 GN B1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;

RL [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-OSTEOSARCOMA;
 RX MEDLINE=99234731; PubMed=10221542;
 RA Adams A.E., Kosorblatt M., Suva L.J.;
 RT "Identification of a novel parathyroid hormone-responsive gene in
 human osteoblastic cells.";
 RL Bone 24:305-313(1999).
 DR EMBL: AF095771; AAD25981.1; -
 SQ SEQUENCE 802 AA; 89.644 MW: 30785141.22434322 GC664;

Query Match 55.0% Score 39; DB 4; Length 802;
 Best Local Similarity 72.7% Pred. No. 114+00;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY 2 EELMLRLQDYE 12
 I:|||||
 Db 530 EELMLRLQDYE 540

RESULT 15

Q9C6K2 PRELIMINARY; PROT; 86 AA.

AC Q9C6K2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Hypothetical 10.0 kDa protein.
 GN P8A12.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Curosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RL [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_ COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White B., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 Bucher E., Chan A., Chao Q., Chen H., Cheung R.F., Chin C.W.,
 Chong M.K., Glonek L., Gonyea A.B., Gonyea A.E., Gonyea T.B., Gonyea K.,
 Dunn P., Elqu P., Feldblum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 Hunter J.R., Jenkins J., Johnson-Hopson C., Khan S., Khaykin R.,
 Kim C.J., Koh H.J., Krometskaia I., Kurtz D.H., Kwan A., Lam B.,
 Langin Hooper S., Lee A., Lee J.M., Lee C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Martelli A.,
 Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Faj G., Peterkofsky A., Pines F.K., Rhee M., Rooney T., Rowley D.,
 Sakano H., Salzman S., Schwartz J.P., Shinn P., Southwick A.M.,
 Sun H., Talbot J.J., Lambunga G., Toriumi M.J., Town C.D.,
 Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000)
 DR EMBL: AC092884; AAC50944.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 86 AA; 10022 MW: 6718869423E84B GC664;

Query Match 53.5% Score 48; DB 10; Length 86;
 Best Local Similarity 58.3% Pred. No. 17;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Caps 0;

QY 1 EELMLRLQDYE 12
 I:|||||
 Db 67 EDVMLPKEDYE 78

Search completed: January 16, 2003, 16:55:44
 Job time : 44.7143 secs

